OIPE

```
            RAW SEQUENCE LISTING              DATE: 07/18/2001
            PATENT APPLICATION:  US/09/896,791  TIME: 13:15:34

            Input Set : A:\00244-WO.txt
            Output Set: N:\CRF3\07182001\I896791.raw

    4 <110> APPLICANT: Berkenstam
    6 <120> TITLE OF INVENTION: Screening methods
    8 <130> FILE REFERENCE: 00244
C-  10 <140> CURRENT APPLICATION NUMBER: US/09/896,791
C-  11 <141> CURRENT FILING DATE: 2001-06-29
   13 <160> NUMBER OF SEQ ID NOS: 3
   15 <170> SOFTWARE: PatentIn Ver. 2.1
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Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 460
   19 <212> TYPE: DNA
   20 <213> ORGANISM: Mus musculus
   22 <300> PUBLICATION INFORMATION:
   23 <308> DATABASE ACCESSION NO: GenBank / AA028416
   24 <309> DATABASE ENTRY DATE: 1996-09-16
   26 <400> SEQUENCE: 1
   27 gccatggcgt tggggctgca gcgcgtgagg tcgaacaccg agctgcggaa ggagaagtcg 60
   28 cgggaccgcc cgcagccggc gcacgaggag acggaggtgc tgtaccagct ggcgcacact 120
E--> 29 ctgccctttg cgcgcggcgt cacacc ntc tggacaaggc ctccatcatg cgcctcacaa 180
E--> 30 tcagctacct gcgcatgacc gcctctgcgc acaga tgga aaaggggga gagccactgg 240
   31 acgcctgcta cctgaaggcc ctggaggGtt tcgtcatggt actcaccgcc gaggagacaa 300
   32 tggcttacct gtcggaaaat gtcagcaagc acctgggcct cagtcagtgg acctctgttc 360
   33 ctcctccctg atacataacc ccactcctgg taccaatttc tctctggagc tcattggaca 420
   34 cagtatcttt gatttttatca tccctgtgac caagaggaac               460
  134 <210> SEQ ID NO: 3
  135 <211> LENGTH: 307
  136 <212> TYPE: PRT
  137 <213> ORGANISM: Mus musculus
  139 <400> SEQUENCE: 3
  140 Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn Thr Glu Leu Arg Lys
  141  1               5                  10                  15
  142 Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu
  143               20                  25                  30
  144 Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser
  145           35                  40                  45
  146 Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu
  147       50                  55                  60
  148 Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys Arg Gly Arg Ala Thr
  149  65                  70                  75                  80
  150 Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe Arg His Gly Thr His
  151               85                  90                  95
  152 Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys Cys Gln Gln Ala Pro
  153              100                 105                 110
  154 Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser Leu Ile His Asn Pro
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/896,791

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Input Set : A:\00244-WO.txt
Output Set: N:\CRF3\07182001\I896791.raw

```
155           115                  120                  125
156 Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile Gly His Ser Ile Phe
157     130                  135                  140
158 Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr
159 145                  150                  155                  160
160 Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu Ala Pro Thr Glu Arg
161                  165                  170                  175
162 His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr
163           180                  185                  190
164 Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu His Cys Ser Gly His
165           195                  200                  205
166 Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro
167     210                  215                  220
168 Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile
169 225                  230                  235                  240
170 Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu Gly Leu Pro Gln Glu
171                  245                  250                  255
172 Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu Trp Lys Ala Leu Leu
173           260                  265                  270
174 Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu Gln Gly Lys Gly Thr
175           275                  280                  285
176 Glu Ser Ser Leu Pro Ser Trp Val Leu Trp Ala Leu Asn Arg Lys Asn
177     290                  295                  300
178 Cys Pro Gly
179 305
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E--> 184 00244-WO
E--> 187 - 1 -

delete

VERIFICATION SUMMARY   DATE: 07/18/2001
PATENT APPLICATION: US/09/896,791   TIME: 13:15:35

      Input Set : **A:\00244-WO.txt**
      Output Set: **N:\CRF3\07182001\I896791.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:184 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/896,791

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
      prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
      ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
      each n or Xaa can only represent a single residue. Please present the maximum number of each
      residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
      the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
      Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      This sequence is intentionally skipped

      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
      <400> sequence id number
      000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
      In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
      is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
      "Unknown." Please explain source of genetic material in <220> to <223> section.
      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING ERROR REPORT
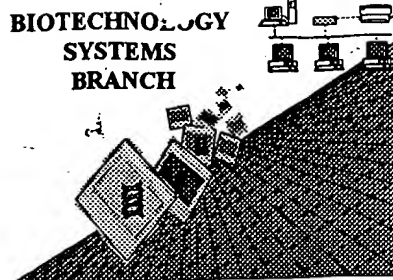
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/896,791_

Source: _OIPE_

Date Processed by STIC: _7/18/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker